

Blast 2 Sequence:

Exhibit 3

NCBI **Entrez** **BLAST 2 sequences** **BLAST** **Example** **Help**

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site.
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program blastn Matrix Not Applicable

Parameters used in BLASTN program only:

Reward for a match: 1 Penalty for a mismatch: 2
 Use Mega B AST Strand option Both strands

Open gap 5 and extension gap 2 penalties
 gap x_dropoff 50 expect 10 word size 11 Filter

Sequence 1 Enter accession or GI 13027635 or download from file
 or sequence in FASTA format from: to:

Sequence 2 Enter accession or GI or download from file
 or sequence in FASTA format from: to:
 cgaccaagtctatcagcgcttccgggt

Comments and suggestions to: blast-help@ncbi.nlm.nih.gov
 Credits to: Tatiana Tatusov and Tom Madden

Blast Result



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: 1 Mismatch: 2 gap open: 5 gap extension: 2
x_dropoff: 50 expect: 10.000 wordsize: 11 Filter Align

Sequence gi 1 1307635 Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA Length 2753

Sequence lcl|seq_2 2 Length 25

No significant similarity was found